

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/562,942
Source: IFWP
Date Processed by STIC: 1/10/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/10/2006

PATENT APPLICATION: US/10/562,942

TIME: 08:53:10

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J562942.raw

3 <110> APPLICANT: DOI, Hirofumi
 4 SAITO, Ken
 6 <120> TITLE OF INVENTION: Inhibition of Nerve Cell Death by Inhibiting Degradation of
 SHC3, ATF6 or
 7 CREBL1 by HtrA2 and Method of Ameliorating Neurodegenerative Diseases
 9 <130> FILE REFERENCE: 3190-088
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/562,942
 12 <141> CURRENT FILING DATE: 2005-12-29
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/014378
 15 <151> PRIOR FILING DATE: 2004-09-30
 17 <150> PRIOR APPLICATION NUMBER: JP P2003-342588
 18 <151> PRIOR FILING DATE: 2003-09-30
 20 <160> NUMBER OF SEQ ID NOS: 37
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1377
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature
 31 <223> OTHER INFORMATION: DNA that codes for HtrA2 precursor protein
 34 <400> SEQUENCE: 1
 35 atggctgctgc cgagggcgagg gcggggtgca ggctggagcc ttcggggcatg gcgggctttg 60
 37 gggggcattc gctgggggag gagaccccggt ttgacccttg acctccgggc cctgctgacg 120
 39 tcaggaaactt ctgacccccg gggccgagtg acttatggga ccccgagctt ctgggcccgg 180
 41 ttgtctgttg gggtcactga accccgagca tgcctgacgt ctgggacccc ggggtccccg 240
 43 gcacaactga ctgcggtgac ccagataacc aggacccggg aggcctcaga gaactctgga 300
 45 acccggttcgc gcgcgtggct ggcggtggcg ctgggcgctg ggggggcagt gctgttgttg 360
 47 ttgtggggcg ggggtcgggg tcttcgggcc gtcttcgccc cgtccctag cccgcccgcc 420
 49 gcttctcccc ggagtcagta caacttcac gcagatgtgg tggagaagac agcacctgcc 480
 51 gtgggtctata tcgagatcct ggaccggcac ctttctcttg gccgcgaggt ccctatctcg 540
 53 aacggctcag gattcgtggt ggctgccgat gggctcattg tcaccaacgc ccatgtggtg 600
 55 gctgatcggc gcagagtcgg tgtgagactg ctaagcggcg acacgtatga ggccgtggtc 660
 57 acagctgtgg atcccgtggc agacatcgca acgctgagga ttcagactaa ggagcctctc 720
 59 cccacgctgc ctctgggacg ctgagctgat gtccggcaag gggagtttgt tgttgccatg 780
 61 ggaagtcctt ttgactgca gaacacgatc acatccggca ttgttagctc tgctcagcgt 840
 63 ccagccagag acctgggact cccccaacc aatgtggaat acattcaaac tgatgcagct 900
 65 attgattttg gaaactctgg aggtcccctg gttaacctgg atggggaggt gattggagtg 960
 67 aacaccatga aggtcacagc tggaatctcc tttgccatcc cttctgatcg tcttcgagag 1020
 69 tttctgcatc gtggggaaaa gaagaattcc tcttcgggaa tcagtgggtc ccagcggcgc 1080
 71 tacattgggg tgatgatgct gaccctgagt ccagcatcc ttgctgaact acagcttcga 1140
 73 gaaccaagct ttcccgatgt tcagctggtt gtactatccc ataaagtcac cctgggctcc 1200
 75 cctgcacacc gggctgggtc gcggcctggg gatgtgattt tggccattgg ggagcagatg 1260
 77 gtacaaaatg ctgaagatgt ttatgaagct gttcgaacct aatcccagtt ggcagtgcag 1320

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79 atccggcgagg gacgagaaac actgacctta tatgtgaccc ctgaggtcac agaatga      1377
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 458
84 <212> TYPE: PRT
85 <213> ORGANISM: Homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <223> OTHER INFORMATION: HtrA2 precursor protein
92 <400> SEQUENCE: 2
94 Met Ala Ala Pro Arg Ala Gly Arg Gly Ala Gly Trp Ser Leu Arg Ala
95 1      5      10      15
98 Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr
99      20      25      30
102 Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala
103      35      40      45
106 Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly
107      50      55      60
110 Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg
111 65      70      75      80
114 Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser
115      85      90      95
118 Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly
119      100     105     110
122 Ala Gly Gly Ala Val Leu Leu Leu Leu Trp Gly Gly Gly Arg Gly Pro
123      115     120     125
127 Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg
128      130     135     140
131 Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala
132 145     150     155     160
135 Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu
136      165     170     175
139 Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu
140      180     185     190
143 Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val
144      195     200     205
147 Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp
148      210     215     220
151 Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu
152 225     230     235     240
155 Pro Thr Leu Pro Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe
156      245     250     255
159 Val Val Ala Met Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser
160      260     265     270
163 Gly Ile Val Ser Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro
164      275     280     285
167 Gln Thr Asn Val Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly
168      290     295     300
171 Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val
172 305     310     315     320

```

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```

175 Asn Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp
176           325           330           335
179 Arg Leu Arg Glu Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser
180           340           345           350
183 Gly Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr
184           355           360           365
187 Leu Ser Pro Ser Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe
188           370           375           380
191 Pro Asp Val Gln His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser
192 385           390           395           400
195 Pro Ala His Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile
196           405           410           415
199 Gly Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg
200           420           425           430
203 Thr Gln Ser Gln Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu
204           435           440           445
207 Thr Leu Tyr Val Thr Pro Glu Val Thr Glu
208           450           455

```

211 <210> SEQ ID NO: 3

212 <211> LENGTH: 981

213 <212> TYPE: DNA

214 <213> ORGANISM: Homo sapiens

216 <220> FEATURE:

217 <221> NAME/KEY: misc_feature

218 <223> OTHER INFORMATION: DNA that codes for mature HtrA2

221 <400> SEQUENCE: 3

```

222 atggcgcgtcc ctagcccgcc gcccgccttct ccccgaggatc agtacaactt catcgcagat      60
224 gtgggtggaga agacagcacc tgccgtgggtc tatatcgaga tcctggaccg gcaccctttc      120
226 ttggggccgcg aggtccctat ctggaacggc tcaggattcg tgggtggctgc cgatgggctc      180
228 attgtcacca acgcccattg ggtggctgat cggcgcagag tccgtgtgag actgctaagc      240
230 ggcgacacgt atgaggccgt ggtcacagct gtggatcccg tggcagacat cgcaacgctg      300
232 aggattcaga ctaaggagcc tctccccacg ctgcctctgg gacgctcagc tgatgtccgg      360
234 caaggggaggt ttgttgttgc catgggaagt ccctttgcac tgcagaacac gatcacatcc      420
236 ggcattgtta gctctgctca gcgtccagcc agagacctgg gactccccca aaccaatgtg      480
238 gaatacattc aaactgatgc agctattgat tttggaaact ctggagggtcc cctggttaac      540
240 ctggatgggg aggtgattgg agtgaacacc atgaagggtc cagctggaat ctcctttgcc      600
242 atcccttctg atcgtcttcg agagtttctg catcgtgggg aaaagaagaa ttcctcctcc      660
244 ggaatcagtg ggtcccagcg gcgctacatt ggggtgatga tgctgaccct gagtcccagc      720
246 atccttgctg aactacagct tcgagaacca agctttcccg atgttcagca tgggtgtactc      780
248 atccataaag tcatcctggg ctcccctgca caccgggctg gtctgcgggc tgggtgatgtg      840
250 attttggcca ttggggagca gatggtacaa aatgctgaag atgtttatga agctgttcga      900
252 acccaatccc agttggcagt gcagatccgg cggggacgag aaacactgac cttatatgtg      960
254 acccctgagg tcacagaatg a
255                                     981

```

257 <210> SEQ ID NO: 4

258 <211> LENGTH: 326

259 <212> TYPE: PRT

260 <213> ORGANISM: Homo sapiens

262 <220> FEATURE:

263 <221> NAME/KEY: misc_feature

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264 <223> OTHER INFORMATION: mature HtrA2

267 <400> SEQUENCE: 4

```

269 Met Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg Ser Gln Tyr Asn
270 1          5          10          15
273 Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile
274          20          25          30
277 Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser
278          35          40          45
281 Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn
282          50          55          60
285 Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val Arg Leu Leu Ser
286 65          70          75          80
289 Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp
290          85          90          95
293 Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro
294          100         105         110
297 Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met
298          115         120         125
301 Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser Gly Ile Val Ser
302          130         135         140
305 Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro Gln Thr Asn Val
306 145         150         155         160
309 Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly Asn Ser Gly Gly
310          165         170         175
313 Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val Asn Thr Met Lys
314          180         185         190
317 Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp Arg Leu Arg Glu
318          195         200         205
321 Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser Gly Ile Ser Gly
322          210         215         220
325 Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr Leu Ser Pro Ser
326 225         230         235         240
329 Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe Pro Asp Val Gln
330          245         250         255
333 His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser Pro Ala His Arg
334          260         265         270
337 Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile Gly Glu Gln Met
338          275         280         285
341 Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg Thr Gln Ser Gln
342          290         295         300
345 Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu Thr Leu Tyr Val
346 305         310         315         320
349 Thr Pro Glu Val Thr Glu
350          325

```

353 <210> SEQ ID NO: 5

354 <211> LENGTH: 981

355 <212> TYPE: DNA

356 <213> ORGANISM: Artificial

358 <220> FEATURE:

RAW SEQUENCE LISTING

DATE: 01/10/2006

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TIME: 08:53:10

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J562942.raw

359 <223> OTHER INFORMATION: Polynucleotide consisting of the same base sequence of SEQ ID NO:

360 3 wherein the nucleotide of position 520 is g

362 <220> FEATURE:

363 <221> NAME/KEY: misc_feature

364 <223> OTHER INFORMATION: DNA that codes for mature HtrA2(S306A)

367 <400> SEQUENCE: 5

```

368 atggcgcgtcc ctagcccgcc gcccgccttct ccccgaggatc agtacaaactt catcgcagat      60
370 gtgggtggaga agacagcacg tgccgtgggtc tatatcgaga tcctggaccg gcaccctttc      120
372 ttgggcccgcg aggtccctat ctggaacggc tcaggattcg tgggtggctgc cgatgggctc      180
374 attgtcacca acgcccattg ggtggctgat cggcgagag tccgtgtgag actgctaagc      240
376 ggcgacacgt atgaggccgt ggtcacagct gtggatcccc tggcagacat cgcaacgctg      300
378 aggattcaga ctaaggagcc tctccccacg ctgcctctgg gacgctcagc tgatgtccgg      360
380 caaggggagt ttgttgttgc catgggaagt ccctttgcac tgcagaacac gatcacatcc      420
382 ggcattgtta gctctgctca gcgtccagcc agagacctgg gactccccca aaccaatgtg      480
384 gaatacattc aaactgatgc agctattgat ttgggaaacg ctggagggtc cctggttaac      540
386 ctggatgggg aggtgattgg agtgaacacc atgaagggtc cagctggaat ctccctttgcc      600
388 atcccttctg atcgtcttcg agagtttctg catcgtgggg aaaagaagaa ttcctcctcc      660
390 ggaatcagtg ggtcccagcg gcgctacatt ggggtgatga tgctgaccct gagtcccagc      720
392 atccttctg aactacagct tcgagaacca agctttcccg atgttcagca tgggtgtactc      780
394 atccataaag tcatcctggg ctcccctgca caccgggctg gtctgcggcc tgggtgatgtg      840
396 attttggcca ttggggagca gatggtacaa aatgctgaag atgtttatga agctgttcga      900
398 acccaatccc agttggcagt gcagatcccg cggggacgag aaacactgac cttatatgtg      960
400 acccctgagg tcacagaatg a                                     981

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403 <210> SEQ ID NO: 6

404 <211> LENGTH: 326

405 <212> TYPE: PRT

406 <213> ORGANISM: Artificial

408 <220> FEATURE:

409 <223> OTHER INFORMATION: Polypeptide consisting of the same amino acid sequence of SEQ ID

410 NO:4 wherein the 174th amino acid residue is substituted by Ala

412 <220> FEATURE:

413 <221> NAME/KEY: misc_feature

414 <223> OTHER INFORMATION: mature HtrA2(S306A)

417 <400> SEQUENCE: 6

```

419 Met Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg Ser Gln Tyr Asn
420 1          5          10          15
423 Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile
424          20          25          30
427 Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser
428          35          40          45
431 Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn
432          50          55          60
435 Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val Arg Leu Leu Ser
436 65          70          75          80
439 Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp
440          85          90          95
443 Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro
444          100         105         110
447 Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/10/2006
PATENT APPLICATION: US/10/562,942 TIME: 08:53:11

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J562942.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36
Seq#:37

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/562,942

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Output Set: N:\CRF4\01102006\J562942.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number